Applicants: Rolando Pajon Feyt, et al.
Serial No.: 10/580,888
Filing Date: May 25, 2006
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Response to non-final office action issued February 8, 2008
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Amendment to the Specification

Please delete lines 25-26 on page 12 of the specification and replace it with the following:

~~Identificación del producto del gen nmb0928 como la lipoproteína-34 de Neisseria~~
~~meningitidis~~

Identification of the NMB0928 protein as the lipoprotein-34 (NlpB) of Neisseria
meningitides

Please delete the paragraph on page 12, lines 14-18, and replace it with the following:

Identification of proteins based on the mass spectra was carried out with the MASCOT
program (Perkins DN, *et al.* 1999. *Probability-based protein identification by searching
sequence databases using mass spectrometry data.* Electrophoresis 20:3551-3567.
~~http://www.matrixscience.com/~~ http://www.matrixscience.com/). Search parameters included
cysteine modifications as well as oxidations and deamidations.

Please delete the paragraph on page 14, lines 4-5, and replace it with the following:

For the prediction of signal peptide the SignalP World Wide Web server
(~~http://www.cbs.dtu.dk/services/SignalP-2.0~~ http://www.cbs.dtu.dk/services/SignalP-2.0)
was employed.

Please delete the paragraph on page 16, lines 19-34, and replace it with the following:

To analyze the conservation of the sequence of the gene codifying for the NMB0928 protein
in the pathogenic species of the Neisseria genus a similarity search with the genomes of
Neisseria meningitidis (serogroups A, B and C) and *Neisseria gonorrhoeae,* annotated in the
NCBI data base, was done (~~NC_003116.1, NC_003112.1, NC_003221, NC_002946~~

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~~SANGER_135720|Contig1~~ NC_003116.1, NC_003112.1, NC_003221, NC_002946 SANGER_135720|Contig1) employing the BLAST program (Altschul SF, et al. 1990. *Basic local alignment search tool.* J Mol Biol 215:403-410. ~~http://www.ncbi.nlm.nih.gov/BLAST/~~ http://www.ncbi.nlm.nih.gov/BLAST/). Figure 8 shows the results of the sequence comparison for those sequences that produce a significant aligment in each of the analyzed genomes. Those sequences have 98% identity in serogroups A and C, 99% identity in serogroup B and 96%identity with *Neisseria gonorrhoeae*, with the sequence obtained for the gene that codicies for the NMB0928 protein (Seq. ID. No. 3). In addition, the sequence of the referred gene was determined for 3 Cuban isolates (Seq. ID. No. 5-7), which belong to serogroup B (B:4:P1.19,15) and a sequence alignment was done by using the ClustalX program (~~http://www.ebi.ac.uk/clustalw/~~ http://www.ebi.ac.uk/clustalw/). The results of the alignment show that there is a great conservation in the nucleotide sequence of the gene NMB0928 among the analyzed strains.